

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Zancope-Oliveia, Rosely M.
et al.,

5 (ii) TITLE OF INVENTION: Nucleic Acids of the M Antigen
Gene of *Histoplasma Capsulatum*, Isolated and
Recombinantly-Produced
Antigens, Vaccines and Antibodies, Method

(iii) NUMBER OF SEQUENCES: 13

10 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fitch, Even, Tabin & Flannery
(B) STREET: 135 South LaSalle Street, Suite 900
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60603-4277

15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

25 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

30 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kaba, Richard A
(B) REGISTRATION NUMBER: 30,562
(C) REFERENCE/DOCKET NUMBER: 6314/62527

35 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-372-7842
(B) TELEFAX: 312-372-7848
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: var. *capsulatum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50 GGATCTGCT GGCTCCGATA ACTTGCTTT ATCCAAGGGT CTCGGCGAAT GCCAGGTGCC
ATCGATCTAT ATTTGAAAGT TTATCACCTC AATGGCTTCA CCCCCATGACG CACCTTTAT
TTTTATTTTC ATTCACTTC TCTGTGGCAA ACATGCAGGT ATGCGAGCTC TGGACCCCTGG

60

120

180

5	GGTGTGGCCC	TTGATGCATA	TGGTTTATTT	ATAGCCGCC	GGAAGCCCTG	GCCTGTTAAA	240
	TTTTGGACCT	CCTCCCGCCA	TTCTTCCAA	ACTTCGTGCG	TCCGTTTCCC	ATTCCCCCCC	300
	TCCCCATTG	GGTTCCTTAT	AGGCCACTGC	GTGCTCCACT	CAAGAAGGGT	CCAGTCAT	360
	TTGGTCTCTA	CCCTCTCCAA	CACTACTGC	ATATGTAATA	TATATCGATA	TCTAACTGCC	420
10	ATTGATTATT	TGTCTTCTC	AGCATCTTT	TGTCTCGAGC	AAGCTTACTC	CACGTTCAAT	480
	TCAGGGGTA	AAAATGCGGT	CGCTCAAGCT	TATACTCGCC	TCGGCGGGTG	TTGTTTCTGC	540
	AGCCTGTCCC	TACATGTCA	GGGAGATGCC	TAGCGGGTCA	AAAGGCCCCC	TGATCGCCG	600
	CCATGACACT	CTCTCCGACC	CTACGCCAAC	GTTCCTTAGC	AAGTTTACA	TTGACGATGA	660
	ACAGTCGGT	CTAACAAACCG	ACGTGGGTGG	TTCCCATCGC	GACCAACACA	GCCTGAAGGC	720
15	TGAAATAGA	GGGCCAACTC	TACTTGGAGA	TTTTATCTTC	CGCCAGAAAGA	TTCACACCTT	780
	TGATCATGAG	AGGGTATGTA	GATACAAAT	ATGTGACCGT	GTTGCAAATC	CGCTAATTCA	840
	ATTTTACGCA	GGTTCCGTAG	CGCGCCGTCC	ATGCTCGAGG	AGCTGGTGC	CATGGCGTAT	900
	TCACATCCTA	TAATAACTGG	TCGAATATCA	CAGCCGCATC	CTTCTTGAAC	GCGGCAGGAA	960
	AGCAGACACC	AGTATTCTGT	CGGTTTCTA	CAGTCGCTGG	TAGCAGAGGC	AGTGTGACT	1020
20	CTGCTCGCGA	TATCCACGGA	TTTGGCAGCC	GTCTGTATAC	CGATGAAGGC	AATTTGGTA	1080
	AGCATTATAT	CGTGGTAGTC	ATACTCATAA	CAGCACAACA	AATATGAATA	CAAACCCAGG	1140
	ACCTAGGCTG	ACTACTCGGC	AATGTAGATA	TCGTCGGAAA	CAACGTTCCA	GTCTTCTTC	1200
	TTCAGGACGC	TATTCAATT	CCTGATTGTA	TTCACGCTGT	CAAGCCGCAA	CCAGACAGTG	1260
	AAATCCCCA	GGCTGCAACT	GCACATGATA	CGGCATGGGA	TTCCCTCAGC	CAGCAGCCCA	1320
25	GCTCATTGCA	TGCCCCCTTC	TGGGCAATGT	CAGGACATGG	AATCCCTCGC	TCATATGCGTC	1380
	ATGTTGATGG	GTGGGGCGTC	CATACCTTC	GACTTGTAC	CGACGAGGGC	AACTCGACCT	1440
	TGGTCAAGTT	TCGCTGGAA	ACCCCTCAAG	GAAGAGCGGG	CCTGGTATGG	GAAGAGGCAC	1500
	AGGCTCTTGG	CGGAAAGAAAT	CCCGACTTCC	ATCGACAAGA	CCTCTGGGAT	GCCATTGAAT	1560
	CTGGAAGGTA	CCCTGAGTGG	GAGGTAAAGAT	ATGATTCCCC	CAAATCATT	GTCTGACAG	1620
30	TGTTTCTCTG	CTCTGTCGGT	TGCTCTTTTC	GTCTTTTCT	ATATCTCAA	CTAAGACTG	1680
	CTTTATATAC	GTTTTACTCA	TATAGCTGGG	CTTTCATATTG	GTGAATGAAG	CAGATCAATC	1740
	CAAGTTTGAT	TTCGATCTAT	AGATCCCAC	CAAATCATC	CCAGAAGAAC	TTGTTCTTT	1800
	CACCCCAATC	GGAAAAATGG	TCTTGAAACCG	AAACCCAAAA	AGTTATTTG	CGCAAACACTGA	1860
	GCAGATCATG	TTTGGTCCAC	CCCTATATA	TTTGGAAATAT	GAATACATGT	ATAGCTAGAT	1920
35	GAAGCGTATA	TCTAAATATA	TTTCCACAGT	TCCAACAGG	TCATGAGT	CGCGGAATCG	1980
	ATTTCACGGA	TGACCCCTTG	CTTCAGGGCC	GCTTGTACTC	CTACCTGAC	ACTCAATTGA	2040
	ATCGCCATGG	AGGTCCCAAC	TTCGAGCAAC	TGCCGATCAA	CAGACCCCGC	ATCCCCATTCC	2100
	ATAACAAACAA	TCGCGACGGT	GCTGGTAAGC	TACTTCTC	CTACCATGTC	AACTCCATC	2160
40	TTGACCCAAT	CGATTGTTAT	AGAGTATTAA	CATCCCCGTC	TGACAGGAC	AAATGTTCAT	2220
	CCCTCTAAAC	ACGGCCGCT	ATACACCCAA	CTCAATGAGC	AACGGATTCC	CACAACAAGC	2280
	CAACCGGACC	CATAACAGAG	GATTCTTCAC	CGCACCTGGG	CGTATGGTAA	ATGGACCACT	2340
	AGTGCACGAG	CTCAGCCCGA	GCTTCAACGA	CGTCTGGTC	CAACCGCTC	TCTTCTACAA	2400
	CTCACTCACG	GTCTTCGAGA	AGCAATTCT	CGTCAACGCC	ATGCGCTTC	AAAACCTCCA	2460
45	CGTGGGAGT	GAACACGTG	GTAAGAACGT	CATCATCCAG	CTGAACCGCG	TCGACAACGA	2520
	CCTCGCCCGC	CGCGTCGCGC	TAGCTATCGG	CGTCGAACCC	CCATCCCCGG	ACCCAACCTT	2580
	CTACCAACAA	AAGGCAACCG	CCCCCATCGG	ACGAATCTC	TGCGGCTCGA	2640	
	CGGGCTGAAA	ATCGCCCTCC	TGACAAGAGA	CGACGGTAGC	TTCACGATCG	CGGAGCAGCT	2700
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	CGTGTACGTC	GTGCGCGGCC	TGCTCACGG	CGCCCTAACG	CAATACCAA	GAGGTGCGCC	2880
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	GCCGGTGTCA	AGCTTCANGA	GGCCTAATT	ATTGGAAGAG	GAGCTTGAAG	TGAAATCTTG	3300
	GTGTAACAT	AAAATTTAT	AATAACTAAT	AACTTATAAT	TAATGTCAT	TGTAATTTC	3360
	TCTCACATT	AATCTATATT	TGATCTTGT	CCTTGTAGC	TGTTAAATA	TAAGCCAAGA	3420
	GAGACAAATA	ATGATAGAT	AACAAATAAT	TGACACCCCA	ATAGGCCTTC	CCTCACGATA	3480
60	TCAGATATT	TCTATCATGT	TGTAATGATA	CCTCAAAAT	GCCACAAGCT	TGCCTGATAT	3540
	TGAATATT	TATGCTGTAA	ATGAGGGAA	GAGCGTACCA	TCCAATAAC	CAGAAAAAAC	3600
	TGTTTAGCT	AAAATCTCA	CTAAGGTCGG	TCGTGTCTAT	TTGAAATGGC	TGCGGCAAGC	3660
	TGACTATCTG	ATAAAAATGT	CTGTATTTCC	GCTTCACGAC	GCATGTTATG	ACTTCGAAT	3720
	ATAGATAAAA	CCTGAACGAT	TTAGCCCCCTG	TTGGGGGAAA	TAGGGTTAG	GGGGCGAGC	3780
	TACATATCAT	TCCCCATATGA	CCAAAAACTA	AAATAGATAT	ATATATATAT	ATATATATAT	3840
	ACAACACCTT	CAAAAAGGAT	CC				3862

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Ser Gly Gln Lys Gly Pro Leu Asp Arg Arg His Asp Thr Leu
 1 5 10 15
 Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu
 5 20 25 30
 Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
 35 40 45
 Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
 50 55 60
 10 Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
 65 70 75 80
 Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
 85 90 95
 15 Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
 100 105 110
 Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
 115 120 125
 Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
 130 135 140
 20 Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
 145 150 155 160
 Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
 165 170 175
 Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
 180 185 190
 Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
 195 200 205
 Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
 210 215 220
 25 Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
 225 230 235 240
 Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
 245 250 255
 Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
 260 265 270
 30 His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
 275 280 285
 Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
 290 295 300
 35 Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
 305 310 315 320
 Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
 325 330 335
 40 Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val
 340 345 350
 Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr
 355 360 365
 Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
 370 375 380
 45 Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
 385 390 395 400
 Asp Gly Ala Gly Gln Met Phe Ile Pro Leu Asn Thr Ala Ala Tyr Thr
 405 410 415
 50 Pro Asn Ser Met Ser Asn Gly Phe Pro Gln Gln Ala Asn Arg Thr His
 420 425 430
 Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu
 435 440 445
 Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
 450 455 460
 55 Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
 465 470 475 480
 Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
 485 490 495
 60 Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
 500 505 510
 Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
 515 520 525
 Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
 530 535 540
 70 Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly

545 550 555 560
Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
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Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg
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Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
595 600 605 610 615 620
Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro
610 615 620 625 630 635 640
10 Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
625 630 635 640 645 650 655
Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
645 650 655 660 665 670 675 680 685
15 Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
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Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
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Asp Gly Leu Thr Ala Tyr Arg Phe Leu Asn Arg Phe Pro Leu Asp Arg
690 695 700
20 Ser Leu Val
705

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

30 Ser Asp Pro Thr Asp Gln Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Asp Phe Ile Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

50 Thr Leu Gln Gly Arg Ala Gly Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe His Arg Gln Asp Leu
1 5 10 15

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: None
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Gly Arg Tyr Pro Glu
1 5

15 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: None
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
1 5 10

25 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ile Ile Pro Glu Glu Leu Val Pro Phe Thr Pro Ile Gly Lys
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other
(ix) FEATURE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AARAAYCCVG AYTTY

15

45 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TTNCCDATNG TRAA

14

(2) INFORMATION FOR SEQ ID NO:12:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

0 (ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGAATCCTC CGACCCTACG GA

22

(2) INFORMATION FOR SEQ ID NO:13:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCAAGCTTC TATCCAACGG GAACCGA

27

09/674195

526 Rec'd PCT/US 26 OCT 2000

1

SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY
THE

DEPARTMENT OF HEALTH AND HUMAN SERVICES CENTERS FOR DISEASE
CONTROL AND

PREVENTION

ZANCOPE-OLIVEIRA, ROSALY M.

LOTT, TIMOTHY J.

MAYER, LEONARD W.

REISS, ERROL

DEEPE, JR., GEORGE S.

<120> NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
HISTOPLASMA CAPSULATUM, ISOLATED AND RECOMBINANTLY-PRODUCED
ANTIGENS, VACCINES AND ANTIBODIES, METHODS AND KITS FOR
DETECTING HISTOPLASMOSES

<130> 65798 / US

<140> NYA

<141> 1999-04-27

<150> U.S. 60/083,676

<151> 1998-04-30

<150> PCT/US99/09151

<151> 1999-04-27

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 3863

<212> DNA

<213> Histoplasma capsulatum

<400> 1

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tctgttttc catctttggatc tgaggtataat ttgcagatat cagtaatattt cgttacgaa	3240
agccgggtgtc aagcttcang aggcctaatt aatttgaaga ggaggttggaa gtgaaatctt	3300
ggtgtacta taataatttta taataactaa taacttataa ttaatgtcta ttgtatattc	3360
ctctcacatt caatctatata ttgatccttgc tccttgcgtt ctgtttaat ataagccaa	3420
agagacaaat aatgtatgtat taacaaataa ttgcacaccc aataggccctt ccctcacgtat	3480
atcagatatt atctatcatg ttgtatgtat acctcaaaaaa tgccacaagc ttgcctgata	3540
ttgaatattt atatgtgtatc aatgttagggaa agagcgtacc atccaaataa ccagaaaaac	3600
atgttttagc ttaaaatctc actaaggctg gtcgtgtcta ttgaaatgg ctgcggcaag	3660
ctgactatct gataaaaaatg tctgttatttgc cgcttcacga cgcatgttac gactttcgaa	3720
tatagataaa acctgttacgat tttggccctt gttggggaa ataggggttta gggggccgg	3780

ctacatatca ttcccatatg accaaaaact aaaatagata tatatatata tatatatata	3840
tacaacacct tcaaaaagga tcc	3863

<210> 2
 <211> 705
 <212> PRT
 <213> *Histoplasma capsulatum*

<400> 2			
Met Pro Ser Gly Gln Lys Gly Pro Leu Asp Arg Arg His Asp Thr Leu			
1	5	10	15
Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu			
20	25	30	
Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His			
35	40	45	
Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile			
50	55	60	
Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg			
65	70	75	80
Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr			
85	90	95	
Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly			
100	105	110	
Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg			
115	120	125	
Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu			
130	135	140	
Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val			
145	150	155	160
Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val			
165	170	175	
Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp			
180	185	190	
Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu			
195	200	205	
Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val			
210	215	220	
Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn			
225	230	235	240
Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly			
245	250	255	
Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe			
260	265	270	
His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu			
275	280	285	
Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe			
290	295	300	
Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val			
305	310	315	320
Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser			
325	330	335	
Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val			

340	345	350
Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr		
355	360	365
Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu		
370	375	380
Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg		
385	390	395
Asp Gly Ala Gly Gln Met Phe Ile Pro Leu Asn Thr Ala Ala Tyr Thr		
405	410	415
Pro Asn Ser Met Ser Asn Gly Phe Pro Gln Gln Ala Asn Arg Thr His		
420	425	430
Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu		
435	440	445
Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg		
450	455	460
Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn		
465	470	475
Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys		
485	490	495
Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg		
500	505	510
Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe		
515	520	525
Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu		
530	535	540
Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly		
545	550	555
Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn		
565	570	575
Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg		
580	585	590
Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala		
595	600	605
Val Ile Val Val Gly Gly Leu Leu Thr Ser Ala Ser Thr Gln Tyr Pro		
610	615	620
Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys		
625	630	635
Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val		
645	650	655
Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly		
660	665	670
Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu		
675	680	685
Asp Gly Leu Thr Ala Tyr Arg Phe Leu Asn Arg Phe Pro Leu Asp Arg		
690	695	700
Ser		
705		

<210> 3
 <211> 8
 <212> PRT
 <213> *Histoplasma capsulatum*

<400> 3
Ser Asp Pro Thr Asp Gln Phe Leu
1 5

<210> 4
<211> 15
<212> PRT
<213> *Histoplasma capsulatum*

<400> 4
Asp Phe Ile Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg
1 5 10 15

<210> 5
<211> 9
<212> PRT
<213> *Histoplasma capsulatum*

<400> 5
Thr Leu Gln Gly Arg Ala Gly Leu Val
1 5

<210> 6
<211> 16
<212> PRT
<213> *Histoplasma capsulatum*

<400> 6
Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe His Arg Gln Asp Leu
1 5 10 15

<210> 7
<211> 6
<212> PRT
<213> *Histoplasma capsulatum*

<400> 7
Ser Gly Arg Tyr Pro Glu
1 5

<210> 8
<211> 10
<212> PRT
<213> *Histoplasma capsulatum*

<400> 8
Phe Asp Phe Asp Leu Leu Asp Pro Thr Lys
1 5 10

<210> 9
<211> 14
<212> PRT

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